CLAIMS

That which is claimed is:

1. A method of modeling a biological system, comprising:

(a) instantiating a plurality of software components; and

(b) connecting each of the plurality of software components to at least one other of the plurality of software components,

wherein data are directly communicated only between software components directly connected to each other.

2. The method of claim 1, wherein step (b) comprises associating one or more input variables of a software component with one or more output variables of another software component.

3. The method of claim 2, wherein the one or more input variables and the one or more output variables each comprise at least one state variable.

4. The method of claim 1, further comprising:

(c) combining a plurality of connected components into a single reusable component.

5. The method of claim 4, wherein the single reusable component is a black box component.

6. The method of claim 1, further comprising:

(c) initializing at least one field of each of the plurality of connected components.

7. The method of claim 6, wherein the value of the at least one field in at least one of the plurality of connected components depends on the value of at least one field in at least one other of the plurality of connected components.

8. The method of claim 7, wherein with respect to each value that depends on the value of at least one field in at least one other connected component, data relating to the dependency is passed to at least one other connected component.

9. The method of claim 8, further comprising:

(d) creating a real ordering representing the order in which the fields will be initialized.

10. The method of claim 2, further comprising:

(c) connecting an adapter to at least one component,

wherein the adapter translates the output of the at least one component from a first format to a second format; and

wherein any other component receiving the output of the at least one component receives the translated value.

11. The method of claim 2, further comprising:

(c) connecting an adapter to at least one component,

wherein the adapter applies a function to the output of the at least one component to map the output from a first value to a second value; and

wherein any other component receiving the output of the at least one component receives the mapped value.

12. The method of claim 2, further comprising:

(c) connecting an adapter to at least one component,

wherein the adapter translates the input of the at least one component from a first format to a second format; and

wherein the component receives the translated value as input.

13. The method of claim 2, further comprising:

(c) connecting an adapter to at least one component,

wherein the adapter applies a function to the input of the at least one component to map the input from a first value to a second value; and

wherein the component receives the mapped value as input.

14. A method in accordance with any of claims 10 through 13, further comprising:

(d) determining whether an output variable of a first component attached to an input variable of a second component can supply to the second component a valid value to the second component;

(e) if the first component cannot supply a valid value, searching in a database of adapters for an adapter that can be connected to either the first component or the second component so as to transform the value of the output variable of the first component to a value that is valid for the second component; and

(f) if an adapter is found, retrieving the adapter and connecting it to the first component or the second component.

15. A method of modeling a biological system, comprising:

connecting each of a plurality of instantiated software components to at least one other of the plurality of software components,

wherein data are directly communicated only between software components directly connected to each other.

16. A system for modeling a biological system, comprising:

means for instantiating a plurality of software components; and

means for connecting each of the plurality of software components to at least one other of the plurality of software components,

wherein data are directly communicated only between software components directly connected to each other.

17. A computer-readable medium having stored thereon computer-executable instructions for performing the steps comprising:

(a) instantiating a plurality of software components; and

(b) connecting each of the plurality of software components to at least one other of the plurality of software components,

wherein data are directly communicated only between software components directly connected to each other.

18. A system for modeling a biological system, comprising:

a processor; and

a memory in communication with said processor,

wherein said processor causes a plurality of software components to be instantiated in said memory;

wherein said processor causes each of the plurality of software components to be connected to at least one other of the plurality of software components;

wherein data are directly communicated only between software components directly connected to each other.

19. A method of modeling a biological system, comprising:

(a) defining and instantiating a software component dynamically; and

(b) subsequently redefining the software component.

20. The method of claim 19 wherein the software component is defined by prototype.

21. A computer-readable medium having stored thereon a software component relating to a model of a biological system, comprising:

an attribute relating to at least one state variable;

an attribute relating to an initialization method; and

an attribute relating to a method of determining the rate of change over time of the at least one state variable.

22. The software component of claim 21, wherein the at least one state variable comprises a state variable relating to the concentration of a chemical.

23. A computer-readable medium having stored thereon an adapter relating to a model of a biological system, comprising:

an attribute relating to a first data format;

an attribute relating to a second data format; and

an attribute relating to a function for translating data from the first data format to the second data format.

24. A computer-readable medium having stored thereon an adapter relating to a model of a biological system, comprising:

an attribute relating to an expected output variable of a first component;

an attribute relating to an expected input variable of a second component; and

an attribute relating to a function for mapping the value of the output variable to a value that is a valid value for the input variable.

25. A method of evaluating at least one characteristic of a modeled biological system, comprising a plurality of connected software components, the method comprising:

(a) estimating the amount of time necessary to evaluate the at least one characteristic on a first computer;

(b) if the estimated time exceeds a predetermined length of time, selecting a plurality of connected software components that can be evaluated within the predetermined length of time on another computer and that have not previously been selected in any iteration of step (b);

(c) if any software components have been selected in the current iteration of step (b), transmitting to the other computer data relating to the attributes of the selected software components, data indicative of the state of the selected software components, data indicative of the rate of change of the state of the selected software components, and a direction to evaluate the selected software components without reference to the other software components in the modeled biological system;

(d) repeating steps (a) through (c) with respect to the modeled system without any software components previously selected in any iteration of step (b) until the estimated time does not exceed the predetermined length of time;

(e) evaluating any software components not selected in any iteration of step (c) without reference to the other software components in the modeled biological system;

(f) receiving from each other computer to which data was transmitted in any iteration of step (c), data indicative of a rate of change; and

(g) evaluating the entire modeled biological system based on data calculated in step (e) and received in step (f).

26. The method of claim 25, wherein the data relating to the attributes of the selected software components transmitted to the other computer in step (c) are transmitted using a platform independent distributed component-based architecture.

27. The method of claim 25, wherein step (g) comprises (1) dividing the evaluation of the entire modeled biological system into a plurality of tasks, (2) performing at least two of the plurality of tasks in parallel, (3) combining the results of the performed parallel tasks, and (4) performing any of the plurality of tasks not performed in parallel.

28. The method of claim 27, wherein the tasks performed in parallel are performed on separate processors.

29. The method of claim 27, wherein the tasks performed in parallel are performed on separate computers.

30. The method of claim 27, wherein the tasks performed in parallel are performed on separate computers linked together by the Internet.

31. The method of claim 27, wherein the tasks performed in parallel are performed on separate computers running different operating systems.

32. A computer-readable medium having stored thereon computer-executable instructions for performing the steps comprising:

(a) estimating the amount of time necessary to evaluate the at least one characteristic on a first computer;

(b) if the estimated time exceeds a predetermined length of time, selecting a plurality of connected software components that can be evaluated within the predetermined length of time on another computer and that have not previously been selected in any iteration of step (b);

(c) if any software components have been selected in the current iteration of step (b), transmitting to the other computer data relating to the attributes of the selected software components, data indicative of the state of the selected software components, data indicative of the rate of change of the state of the selected software components, and a direction to evaluate the selected software components without reference to the other software components in the modeled biological system;

(d) repeating steps (a) through (c) with respect to the modeled system without any software components previously selected in any iteration of step (b) until the estimated time does not exceed the predetermined length of time;

(e) evaluating any software components not selected in any iteration of step (c) without reference to the other software components in the modeled biological system;

(f) receiving from each other computer to which data was transmitted in any iteration of step (c), data indicative of a rate of change; and

(g) evaluating the entire modeled biological system based on data calculated in step (e) and received in step (f).

33. A method of evaluating at least one characteristic of a modeled biological system, comprising a plurality of connected software components, the method comprising steps for:

(a) estimating the amount of time necessary to evaluate the at least one characteristic on a first computer;

(b) if the estimated time exceeds a predetermined length of time, selecting a plurality of connected software components that can be evaluated within the predetermined length of time on another computer and that have not previously been selected in any iteration of step (b);

(c) if any software components have been selected in the current iteration of step (b), transmitting to the other computer data relating to the attributes of the selected software components, data indicative of the state of the selected software components, data indicative of the rate of change of the state of the selected software components, and a direction to evaluate the selected software components without reference to the other software components in the modeled biological system;

(d) repeating steps (a) through (c) with respect to the modeled system without any software components previously selected in any iteration of step (b) until the estimated time does not exceed the predetermined length of time;

(e) evaluating any software components not selected in any iteration of step (c) without reference to the other software components in the modeled biological system;

(f) receiving from each other computer to which data was transmitted in any iteration of step (c), data indicative of a rate of change; and

(g) evaluating the entire modeled biological system based on data calculated in step (e) and received in step (f).

34. A system for evaluating at least one characteristic of a modeled biological system, comprising a plurality of connected software components, the system comprising:

means for estimating the amount of time necessary to evaluate the at least one characteristic on a first computer;

means for repeatedly selecting a plurality of connected software components that have not been previously selected and that can be evaluated within the predetermined length of time on another computer until all of the unselected components can be evaluated on the first computer within the predetermined length of time;

means for transmitting to each other computer data relating to the attributes of any selected software components, data indicative of the state of the selected software components, data indicative of the rate of change of the state of the selected software components, and a direction to evaluate the selected software components without reference to the other software components in the modeled biological system;

means for evaluating any unselected software without reference to the other software components in the modeled biological system;

means for receiving from each other computer to which data was transmitted, data indicative of a rate of change; and

means for evaluating the entire modeled biological system based on the calculated data and the received data.

35. A system for evaluating at least one characteristic of a modeled biological system, comprising a plurality of connected software components, the system comprising:

a first processor;

a memory in communication with said first processor; and

at least one additional processor in communication with said first processor,

wherein said first processor estimates the amount of time necessary to evaluate the at least one characteristic on a first computer;

wherein, if the estimated time exceeds a predetermined length of time, said first processor selects a plurality of connected software components that can be evaluated within the predetermined length of time on one of said at least one additional processor and that have not previously been selected;

wherein, if any software components have been selected, said first processor causes to be transmitted to the one of said at least one additional processor data relating to the attributes of the selected software components, data indicative of the state of the selected software components, data indicative of the rate of change of the state of the selected software components, and a direction to evaluate the selected software components without reference to the other software components in the modeled biological system;

wherein said first processor evaluates any unselected software components without reference to the other software components in the modeled biological system;

wherein said first processor receives from the one of said at least one additional processor, data indicative of a rate of change; and

wherein said first processor evaluates the entire modeled biological system based on the received data and the calculated data.

36. A system for modeling a biological system, comprising

a plurality of software components, each of which is connected with at least one other software component,

wherein each of said components directly communicates only with parent or child components.

37. The system of claim 36, wherein said components are distributed components in a distributed computing environment.

38. A system for modeling a biological system, comprising

a user interface running on a first computer;

a simulation engine running on a second computer,

wherein said user interface and said simulation engine each comprise at least one distributable component.

39. The system of claim 38, wherein said distributable components are CORBA components.

40. The system of claim 38, wherein said simulation engine includes an ODE solver component.

41. The system of claim 38, wherein said simulation engine includes a solver factory component.

42. The system of claim 38, wherein said simulation engine includes a model factory component.

43. The system of claim 38, wherein said user interface comprises a graphical user interface.

44. The system of claim 38, wherein said user interface comprises one or more of the following components: an XML parsing component; a mathematical equation generation component; and a visualization component.

45. The system of claim 38, wherein said user interface comprises at least two components running on at least two different computers.

46. The system of claim 38, wherein said simulation engine comprises at least two components running on at least two different computers.

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